

IN SILICO

- Identification of testis-specific antigens in the publicly accessible total pool of full-length genes

WET BENCH

- Validation of testis-specificity
- Analysis of testis-specific genes in tumors

Fig. 1

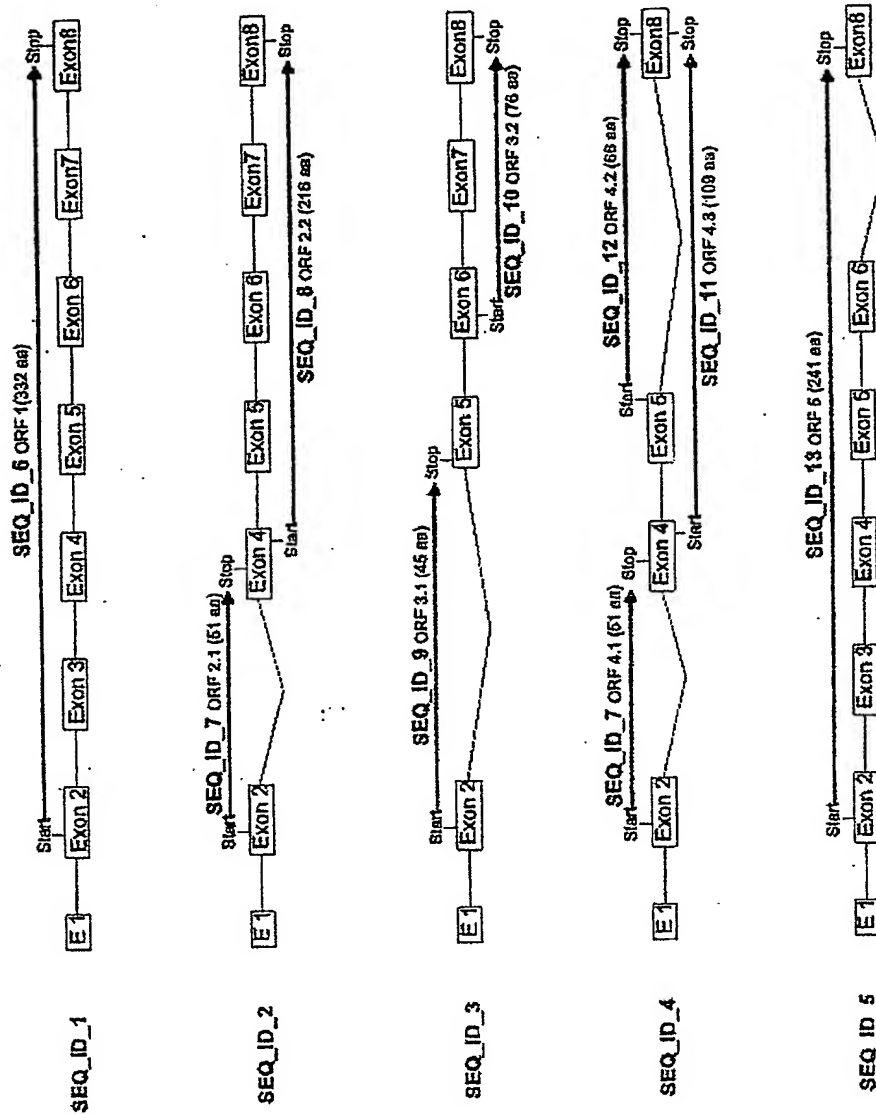


Figure 2

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 SEQ_ID_7 MSTVREQLIEKLLIEDNSQCKITIVGTGAVGACATSIILNLDLDELALVDVAIDKLGEMDLQHSLSFFSTSHTSCKDYSGAHSKIVIVTAGAQ 100
 SEQ_ID_9 MSTVREQLIEKLLIEDNSQCKITIVGTGAVGACATSIILNLDLDELALVDVAIDKLGEMDLQHSLSFFSTSHTSCKDYSGAHSKIVIVTAGAQ 100
 SEQ_ID_8 MSTVREQLIEKLLIEDNSQCKITIVGTGAVGACATSIILNLDLDELALVDVAIDKLGEMDLQHSLSFFSTSHTSCKDYSGAHSKIVIVTAGAQ 100
 SEQ_ID_11 -----
 SEQ_ID_10 -----
 SEQ_ID_12 -----

SEQ_ID_6 QGETKALVQHVVAIAKSIIPATVHYSPDCKILVGNPNVDILTYIWKISGLPVTIVGSCNLDGSAHFYLLIGEKLGVHFTSCHGNI GEGHDS VPL L 200
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 SEQ_ID_8 -----
 SEQ_ID_11 -----
 SEQ_ID_10 -----
 SEQ_ID_12 -----

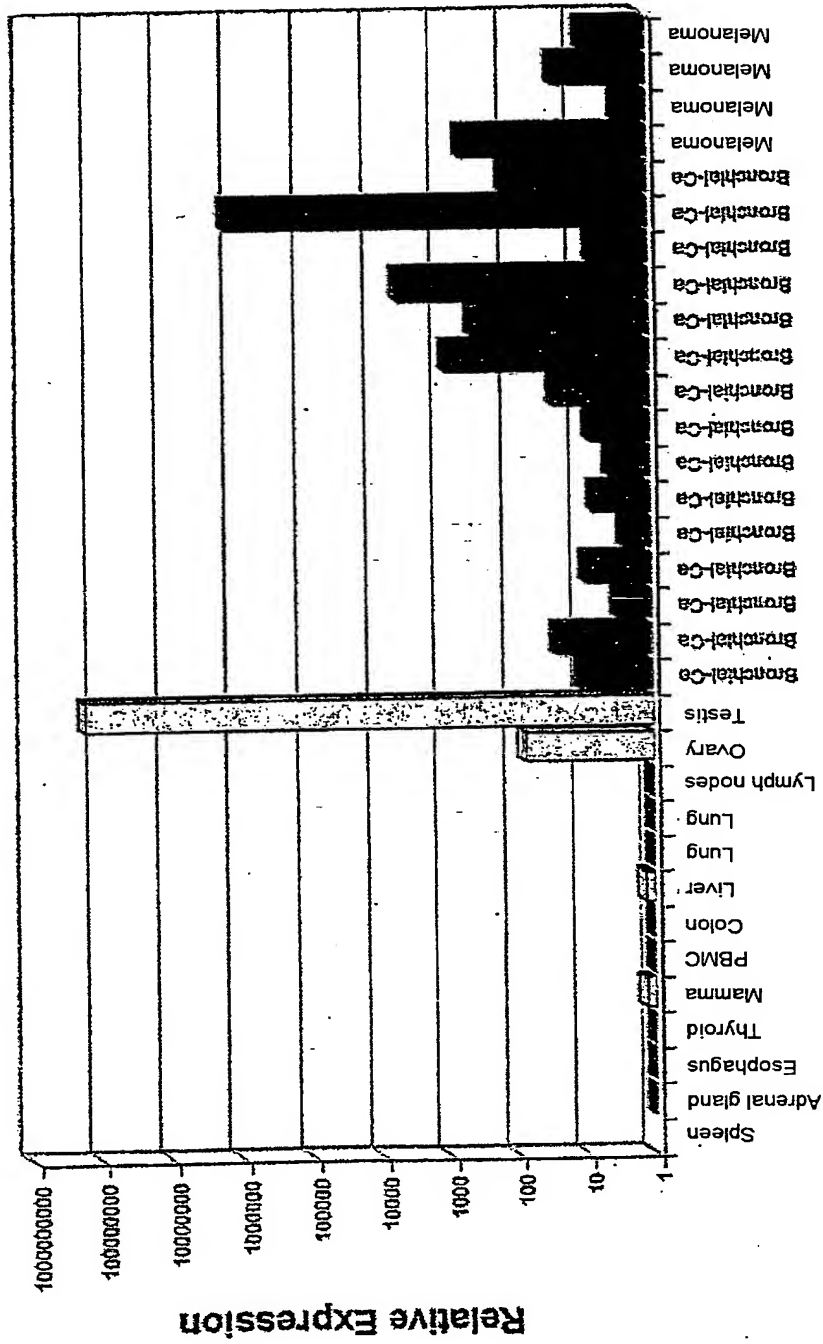
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 SEQ_ID_7 -----
 SEQ_ID_9 -----
 SEQ_ID_8 -----
 SEQ_ID_11 -----
 SEQ_ID_10 -----
 SEQ_ID_12 -----

SEQ_ID_6 SOWVKINLSSEALFKKSAETLWNIQDLIF 332
 SEQ_ID_13 SOWVKINLSSEALFKKSAETLWNIQDLIF 332
 SEQ_ID_7 -----
 SEQ_ID_9 -----
 SEQ_ID_8 SOWVKINLSSEALFKKSAETLWNIQDLIF 216
 SEQ_ID_11 SOWVKINLSSEALFKKSAETLWNIQDLIF 76
 SEQ_ID_10 SOWVKINLSSEALFKKSAETLWNIQDLIF 76
 SEQ_ID_12 SOWVKINLSSEALFKKSAETLWNIQDLIF 66

Lactate dehydrogenase, active site (framed)
 Tumor-specific epitopes (bold type)

Figure 3

LDHC quantitative Real-time PCR



Tissue

Figure 4

TPTE splice variants

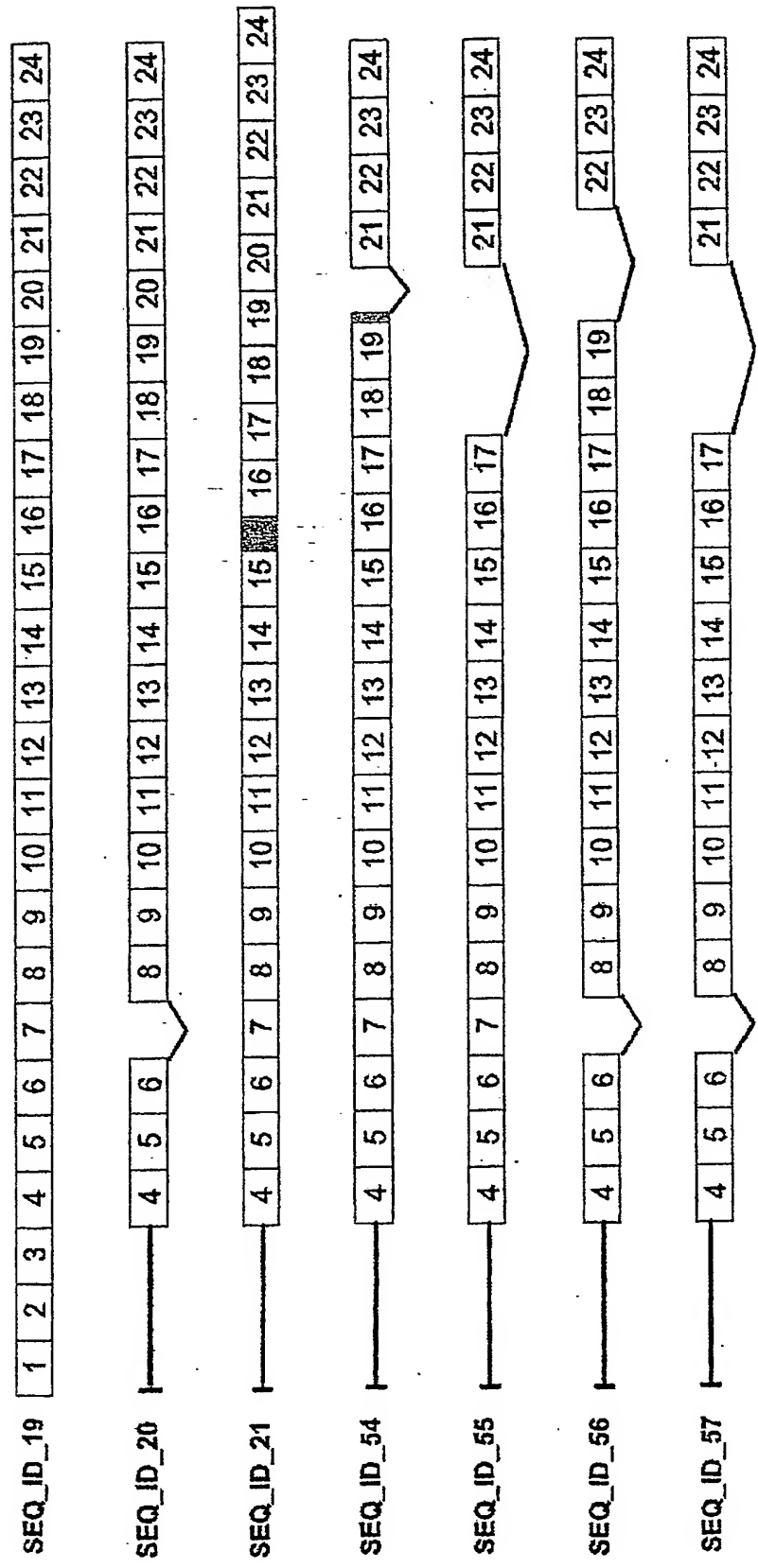


Figure 5

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SEQ_ID_21 MNEFPDPTDLAGVIIELGPNDSPTSEFPGATEEAPAKESPTSEFPGAAARVSPISESVL 60
SEQ_ID_58 MNEFPDPTDLAGVIIELGPNDSPTSEFPGATEEAPAKESPTSEFPGAAARVSPISESVL 60
SEQ_ID_59 MNEFPDPTDLAGVIIELGPNDSPTSEFPGATEEAPAKESPTSEFPGAAARVSPISESVL 60
SEQ_ID_60 MNEFPDPTDLAGVIIELGPNDSPTSEFPGATEEAPAKES-----VL 42
SEQ_ID_61 MNEFPDPTDLAGVIIELGPNDSPTSEFPGATEEAPAKES-----VL 42

SEQ_ID_19 ARLSKFEVEDAENVASYSKIKKIVBSIVSSFAFGLFGVFLVLLDVTLIAOLIFTOSKL 120
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SEQ_ID_21 ARLSKFEVEDAENVASYSKIKKIVBSIVSSFAFGLFGVFLVLLDVTLIAOLIFTOSKL 120
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SEQ_ID_60 ARLSKFEVEDAENVASYSKIKKIVBSIVSSFAFGLFGVFLVLLDVTLIAOLIFTOSKL 102
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SEQ_ID_20 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIIVILLVGVVYIFED 162
SEQ_ID_21 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIIVILLVGVVYIFED 180
SEQ_ID_58 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIIVILLVGVVYIFED 180
SEQ_ID_59 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIIVILLVGVVYIFED 180
SEQ_ID_60 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIIVILLVGVVYIFED 162
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SEQ_ID_21 IKLLRNIPRNTHELRRLRLITLLRIITFLHQKQLEKLIARRVSENKRRYTRDGFOLDIT 240
SEQ_ID_58 IKLLRNIPRNTHELRRLRLITLLRIITFLHQKQLEKLIARRVSENKRRYTRDGFOLDIT 240
SEQ_ID_59 IKLLRNIPRNTHELRRLRLITLLRIITFLHQKQLEKLIARRVSENKRRYTRDGFOLDIT 240
SEQ_ID_60 IKLLRNIPRNTHELRRLRLITLLRIITFLHQKQLEKLIARRVSENKRRYTRDGFOLDIT 222
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SEQ_ID_19 YUTERITAMSPFSSGRQSFYRNFKEVVRFLOKRRNHRYRVYNLCS----- 286
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SEQ_ID_21 YUTERITAMSPFSSGRQSFYRNFKEVVRFLOKRRNHRYRVYNLCSMYITLYCATVDREQ 300
SEQ_ID_58 YUTERITAMSPFSSGRQSFYRNFKEVVRFLOKRRNHRYRVYNLCS----- 286
SEQ_ID_59 YUTERITAMSPFSSGRQSFYRNFKEVVRFLOKRRNHRYRVYNLCS----- 286
SEQ_ID_60 YUTERITAMSPFSSGRQSFYRNFKEVVRFLOKRRNHRYRVYNLCS----- 268
SEQ_ID_61 YUTERITAMSPFSSGRQSFYRNFKEVVRFLOKRRNHRYRVYNLCS----- 268

SEQ_ID_19 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEMMAQOLENIVAIHCKGGT 342
SEQ_ID_20 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEMMAQOLENIVAIHCKGGT 324
SEQ_ID_21 ITARENAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEMMAQOLENIVAIHCKGGT 360
SEQ_ID_58 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEMMAQOLENIVAIHCKGGT 342
SEQ_ID_59 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEMMAQOLENIVAIHCKGGT 342
SEQ_ID_60 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEMMAQOLENIVAIHCKGGT 324
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SEQ_ID_19 DRGTGMCAFLIASEICSTAKESLYYFGERRTDKTHSEKFGQVETPSQKRYVAYFAQVKH 402
SEQ_ID_20 DRGTGMCAFLIASEICSTAKESLYYFGERRTDKTHSEKFGQVETPSQKRYVAYFAQVKH 384
SEQ_ID_21 DRGTGMCAFLIASEICSTAKESLYYFGERRTDKTHSEKFGQVETPSQKRYVAYFAQVKH 420
SEQ_ID_58 DRGTGMCAFLIASEICSTAKESLYYFGERRTDKTHSEKFGQVETPSQKRYVAYFAQVKH 395
SEQ_ID_59 G----- 343
SEQ_ID_60 DRGTGMCAFLIASEICSTAKESLYYFGERRTDKTHSEKFGQVETPSQKRYVAYFAQVKH 370
SEQ_ID_61 G----- 325

SEQ_ID_19 LYNWNLPPRRILFIKRFIYISIPRYVRLDKIQIEMKKVVTSTISLGKCSVLNITTDKI 462
SEQ_ID_20 LYNWNLPPRRILFIKRFIYISIPRYVRLDKIQIEMKKVVTSTISLGKCSVLNITTDKI 444
SEQ_ID_21 LYNWNLPPRRILFIKRFIYISIPRYVRLDKIQIEMKKVVTSTISLGKCSVLNITTDKI 480
SEQ_ID_58 -----YVRDLKIQIEMKKVVTSTISLGKCSVLNITTDKI 379
SEQ_ID_59 -----SYLDNITTDKI 381
SEQ_ID_60 -----YVRDLKIQIEMKKVVTSTISLGKCSVLNITTDKI 361
SEQ_ID_61 -----YVRDLKIQIEMKKVVTSTISLGKCSVLNITTDKI 361

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SEQ_ID_21 LIDVFDGPPLYDDVAVQFFYSMLPTYYDNCSTYFWLHTSFTENNRLYLPANELDNHKKQK 540
SEQ_ID_58 LIDVFDGPPLYDDVAVQFFYSMLPTYYDNCSTYFWLHTSFTENNRLYLPANELDNHKKQK 435
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SEQ_ID_60 LIDVFDGPPLYDDVAVQFFYSMLPTYYDNCSTYFWLHTSFTENNRLYLPANELDNHKKQK 421
SEQ_ID_61 LIDVFDGPPLYDDVAVQFFYSMLPTYYDNCSTYFWLHTSFTENNRLYLPANELDNHKKQK 421

SEQ_ID_19 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 551
SEQ_ID_20 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 533
SEQ_ID_21 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 569
SEQ_ID_58 -----
SEQ_ID_59 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 468
SEQ_ID_60 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 470
SEQ_ID_61 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 450

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Figure 6

[illegible]

Fig. 7a

1	SEQ_31	TGGAAAAATCACA	CTGCTGTGTATATTAACAGGTTACATG	GGATGGAAGACATGTGCAAA	AAAAATCTTGTTC	CCAAAAATCCAGATTC	695
2	SEQ_32	TGGAAAAATCACA	CTGCTGTGTATATTAACAGGTTACATG	GGATGGAAGACATGTGCAAA	AAAAATCTTGTTC	CCAAAAATCCAGATTC	719
3	SEQ_33	TGGAAAAATCACA	CTGCTGTGTATATTAACAGGTTACATG	GGATGGAAGACATGTGCAAA	AAAAATCTTGTTC	CCAAAAATCCAGATTC	674
4	SEQ_29	TGGAAAAATCACA	CTGCTGTGTATATTAACAGGTTACATG	GGATGGAAGACATGTGCAAA	AAAAATCTTGTTC	CCAAAAATCCAGATTC	692
1	SEQ_31	AAATGTGGAGG	GGGCGTCTGCAAGTCTCG	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	784
2	SEQ_32	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	808
3	SEQ_33	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	763
4	SEQ_29	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	781
1	SEQ_31	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	874
2	SEQ_32	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	898
3	SEQ_33	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	853
4	SEQ_29	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	GGGCGTCTCG	AAATGTGGAGG	871
1	SEQ_31	TAGCAGTGC	AGTGTGATATACCA	AAAGACAGG	ATATTA	AAATTAAGG	963
2	SEQ_32	TAGCAGTGC	AGTGTGATATACCA	AAAGACAGG	ATATTA	AAATTAAGG	987
3	SEQ_33	TAGCAGTGC	AGTGTGATATACCA	AAAGACAGG	ATATTA	AAATTAAGG	942
4	SEQ_29	TAGCAGTGC	AGTGTGATATACCA	AAAGACAGG	ATATTA	AAATTAAGG	961
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3	SEQ_33	AGAAAGAGTGTG	TCAGATGTACCA	AGGACAGG	ATATTA	AAATTAAGG	1032
4	SEQ_29	AGAAAGAGTGTG	TCAGATGTACCA	AGGACAGG	ATATTA	AAATTAAGG	1050
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2	SEQ_32	ACGAAGAGTGTG	TCAGATGTACCA	AGGACAGG	ATATTA	AAATTAAGG	1167
3	SEQ_33	ACGAAGAGTGTG	TCAGATGTACCA	AGGACAGG	ATATTA	AAATTAAGG	1122
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2	SEQ_32	AGAAAGAGTGTG	TCAGATGTACCA	AGGACAGG	ATATTA	AAATTAAGG	1257
3	SEQ_33	AGAAAGAGTGTG	TCAGATGTACCA	AGGACAGG	ATATTA	AAATTAAGG	1210
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Fig. 7b

1 SEQ_36	MTVLEITLAVILTLGLALAILLTLRWARKQSEMYISRYSEQSARLLDYEDGGRHAYSHUS	-----ERSHUYTPPTNSLALS	83	
2 SEQ_34	MTVLEITLAVILTLGLALAILLTLRWARKQSEMYISRYSEQSARLLDYEDGGRHAYSHUS	-----ERSHUYTPPTNSLALS	90	
3 SEQ_35	MTVLEITLAVILTLGLALAILLTLRWARKQSEMYISRYSEQSARLLDYEDGGRHAYSHUS	-----ERSHUYTPPTNSLALS	90	
4 NM_006781	MTVLEITLAVILTLGLALAILLTLRWARKQSEMYISRYSEQSARLLDYEDGGRHAYSHUS	-----ERSHUYTPPTNSLALS	90	
1 SEQ_36	SSIALPQGSMSISIKLCIQTTTEPSPRTAGAMQFTAPLP	GATGVINLSQRTIVQTPGPIVQVPGSN	165	
2 SEQ_34	SSIALPQGSMSISIKLCIQTTTEPSPRTAGAMQFTAPLP	GATGVINLSQRTIVQTPGPIVQVPGSN	172	
3 SEQ_35	SSIALPQGSMSISIKLCIQTTTEPSPRTAGAMQFTAPLP	GATGVINLSQRTIVQTPGPIVQVPGSN	180	
4 NM_006781	SSIALPQGSMSISIKLCIQTTTEPSPRTAGAMQFTAPLP	GATGVINLSQRTIVQTPGPIVQVPGSN	170	
1 SEQ_36	SORTASQLAAPYIISQRTARIPQVHTDSSGKITITPVPVLL	FGYNDDELAKKSCKITIILKCGGTARNSQNSHEENKEALKNDIIFTNSVE	256	
2 SEQ_34	SORTASQLAAPYIISQRTARIPQVHTDSSGKITITPVPVLL	FGYNDDELAKKSCKITIILKCGGTARNSQNSHEENKEALKNDIIFTNSVE	262	
3 SEQ_35	SORTASQLAAPYIISQRTARIPQVHTDSSGKITITPVPVLL	FGYNDDELAKKSCKITIILKCGGTARNSQNSHEENKEALKNDIIFTNSVE	270	
4 NM_006781	SORTASQLAAPYIISQRTARIPQVHTDSSGKITITPVPVLL	FGYNDDELAKKSCKITIILKCGGTARNSQNSHEENKEALKNDIIFTNSVE	261	
1 SEQ_36	SLKSAHIKEPHEPREGKGTDLKDKLIGHEVYVDS	DAGIPRQETQLKISEMSI	POGQGAQIRKSVSDVPRGQESQVKKSESGVPRGQEAQVT	343
2 SEQ_34	SLKSAHIKEPHEPREGKGTDLKDKLIGHEVYVDS	DAGIPRQETQLKISEMSI	POGQGAQIRKSVSDVPRGQESQVKKSESGVPRGQEAQVT	352
3 SEQ_35	SLKSAHIKEPHEPREGKGTDLKDKLIGHEVYVDS	DAGIPRQETQLKISEMSI	POGQGAQIRKSVSDVPRGQESQVKKSESGVPRGQEAQVT	360
4 NM_006781	SLKSAHIKEPHEPREGKGTDLKDKLIGHEVYVDS	DAGIPRQETQLKISEMSI	POGQGAQIRKSVSDVPRGQESQVKKSESGVPRGQEAQVT	351
1 SEQ_36	KSGLVVLKQEAQVEKSEMGVPRRQESQVKKSQSGVSKQEAQVKKHESVVLKQEAQVEKSELKVPKQEGQVKEADVPKQEVQEK		435	
2 SEQ_34	KSGLVVLKQEAQVEKSEMGVPRRQESQVKKSQSGVSKQEAQVKKHESVVLKQEAQVEKSELKVPKQEGQVKEADVPKQEVQEK		442	
3 SEQ_35	KSGLVVLKQEAQVEKSEMGVPRRQESQVKKSQSGVSKQEAQVKKHESVVLKQEAQVEKSELKVPKQEGQVKEADVPKQEVQEK		450	
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1 SEQ_36	ESEINGEKSKGRKAKANTGRKYNKKVE	-----	554	
2 SEQ_34	ESEINGEKSKGRKAKANTGRKYNKKVE	-----	561	
3 SEQ_35	ESEINGEKSKGRKAKANTGRKYNKKVE	-----	569	
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Figure 8

MS4A12

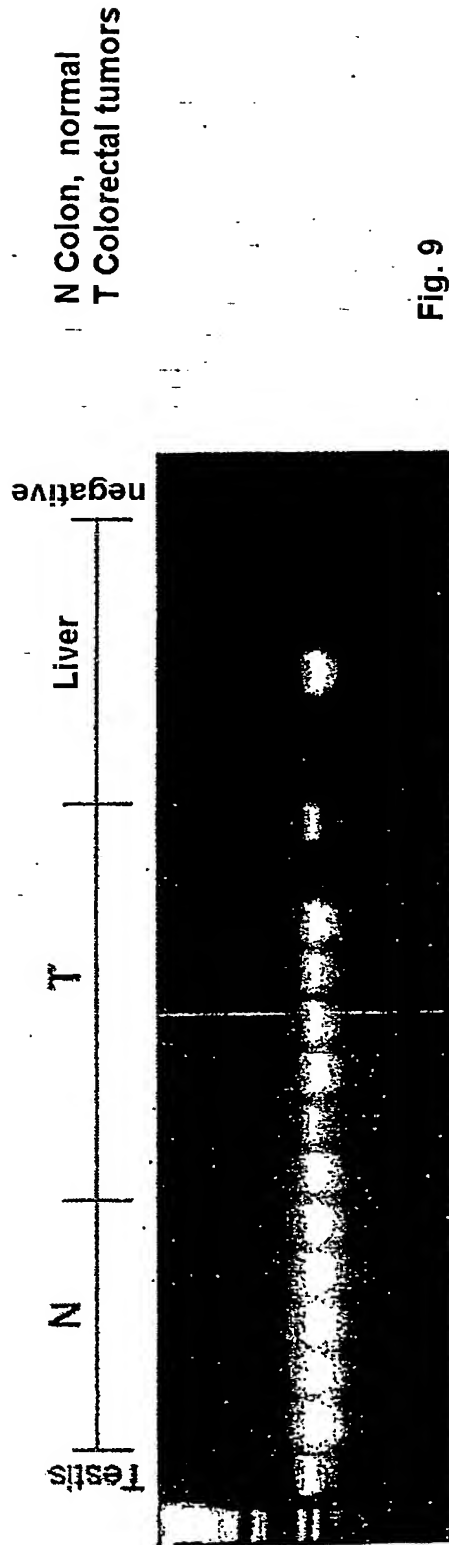


Fig. 9

BRC01

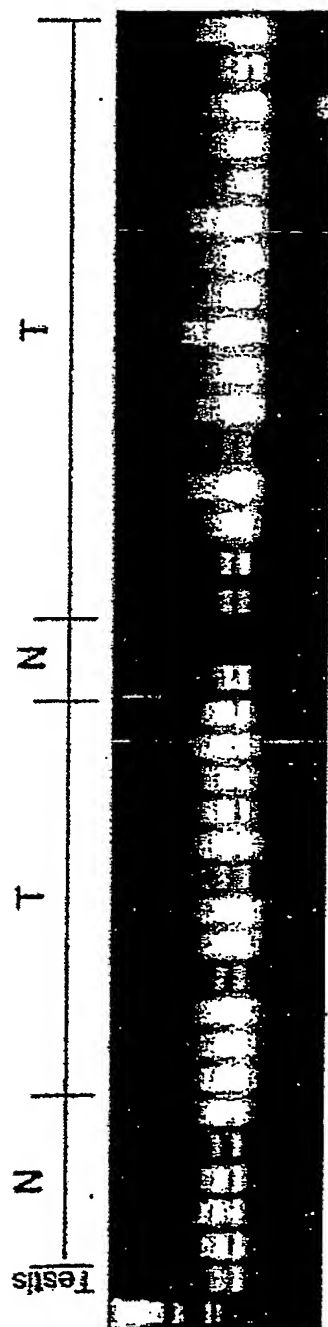
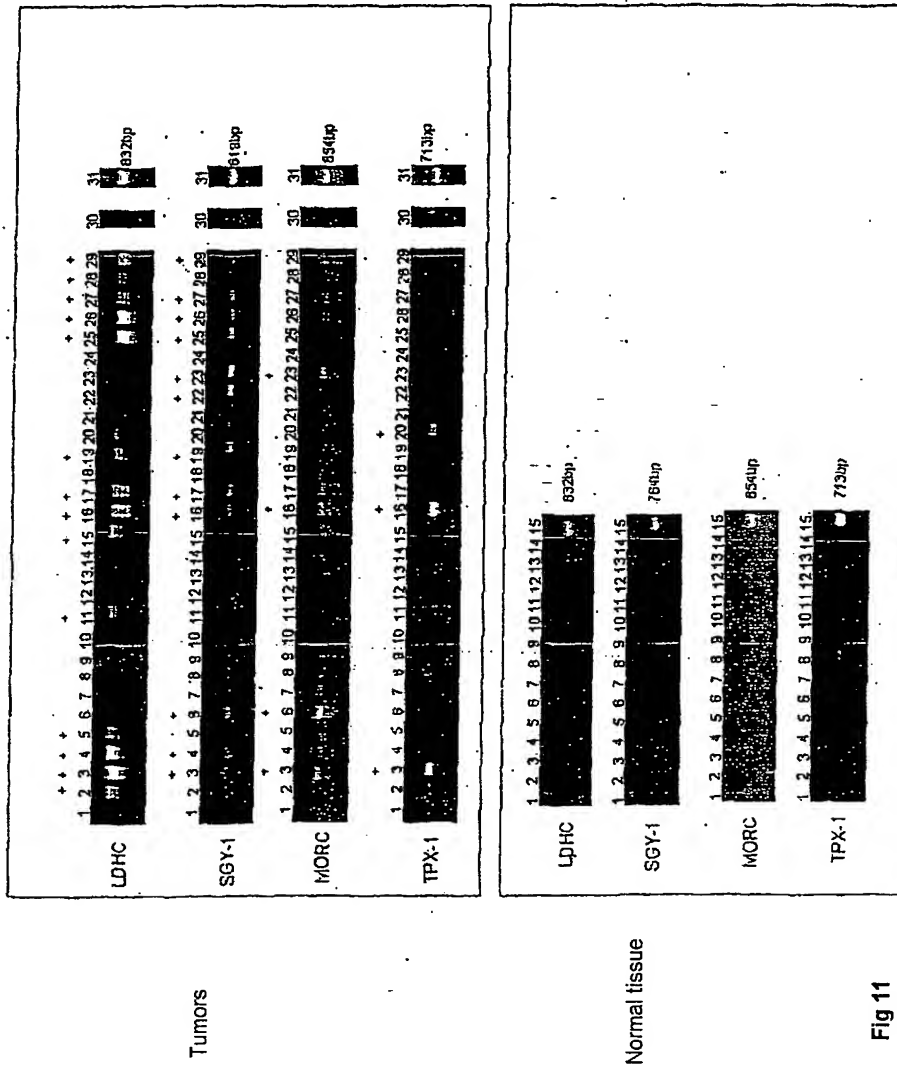
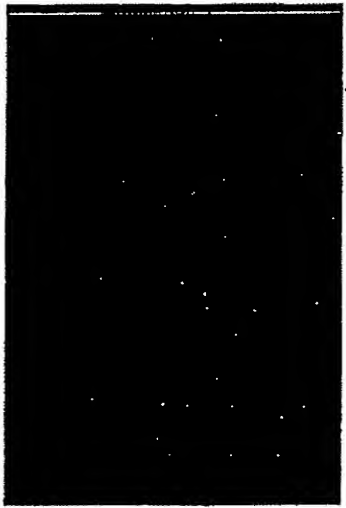
N Breast, normal
T Breast tumors

Fig. 10





anti-cytochrome c



anti-LDHC



Superposition

Fig. 12

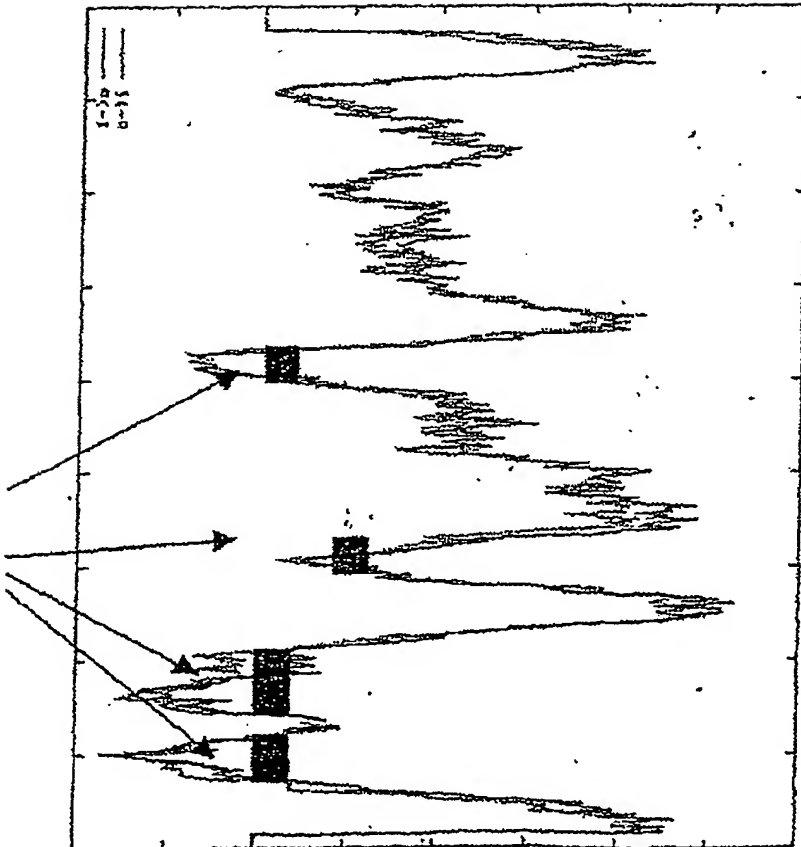
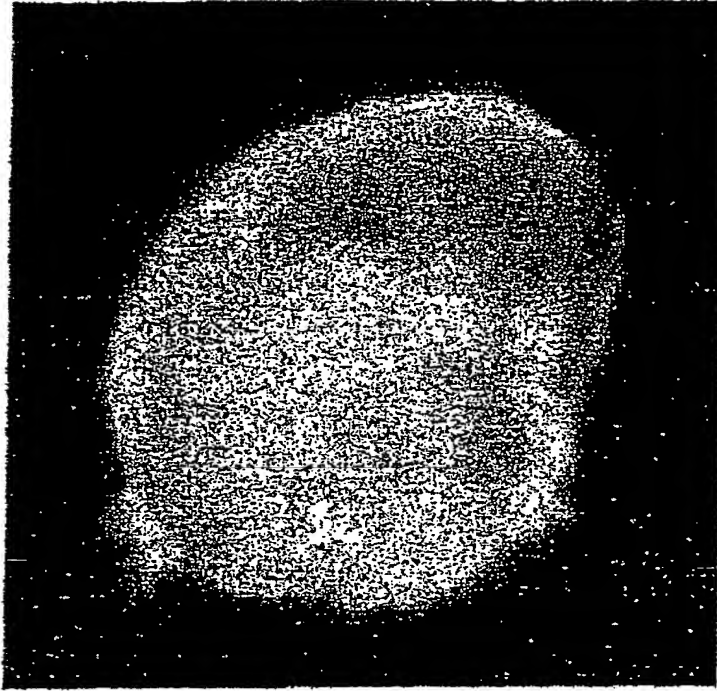


Fig. 13



Fig. 14

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